

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 27, 2003, 17:58:49 : Search time 29 Seconds
(without alignments)
106.576 Million cell updates/sec

Title: US-09-300-612-1

Perfect score: 84

Sequence: 1 LRAMDTPPLWIKTE 15

Scoring table: BLOSSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_21;*

1: sp_archea;*

2: sp_bacteria;*

3: sp_fungi;*

4: sp_human;*

5: sp_invertebrate;*

6: sp_mammal;*

7: sp_mhc;*

8: sp_organelle;*

9: sp_phage;*

10: sp_plant;*

11: sp_rodont;*

12: sp_virus;*

13: sp_vertebrate;*

14: sp_unclassified;*

15: sp_xvirus;*

16: sp_bacteriap;*

17: sp_archeap;*

ALIGNMENTS

RESULT 1
Q9TR78 PRELIMINARY; PRT; 17 AA.
ID Q9TR78;
AC Q9TR78;
DT 01-MAY-2000 (TREMBLref. 13, Created)
DT 01-MAY-2000 (TREMBL. 13, Last sequence update)
DT 01-MAR-2001 (TREMBL. 16, Last annotation update)
DE ANTI-BOTUROPIC complex 48,000 SUBUNIT (Fragment).
OS Didelphis marsupialis (Southern opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorpha; Didelphidae; Didelphis.
OX NCBI_TAXID=9288;
RN [1]
RP SEQUENCE.
RX MEDLINE-05149299; PubMed-7846694;
RA Perles J., Moussetche H., Marangoni S., Oliveira B., Domont G.B.;
RT * Isolation and partial characterization of an anti-botriropic complex
from the serum of South American Didelphidae. *;
RL Toxicon 32:1237-1249(1994).
SQ SEQUENCE 17 AA; 1947 MW; CB55FB40E73B2A2A CRC64;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	84	100.0	17	6 Q9TR78	Q9tr78 didelphis m
2	46	54.8	729	5 Q9VOP3	Q9vop3 drosophila
3	46	54.8	856	5 Q9GZ10	Q9gz10 drosophila
4	46	54.8	1219	5 Q9VT64	Q9vt64 drosophila
5	46	54.8	1221	5 Q8SZR7	Q8szr7 drosophila
6	45	53.6	97	12 Q91P83	Q91p83 tomato leaf
7	45	53.6	97	12 Q91ME9	Q91me9 pepper leaf
8	45	53.6	312	6 Q9N126	Q9n126 bos taurus
9	44	52.4	125	4 Q9NV61	Q9nv61 homo sapien
10	44	52.4	377	16 Q9V632	Q9v632 rhizobium m
11	44	52.4	695	17 Q9UG1	Q9ug1 pyrococcus
12	44	52.4	1327	4 Q15070	Q15070 homo sapien
13	43	51.2	278	10 Q94688	Q94688 oryza sativ
14	43	51.2	354	2 Q8VM74	Q8vm74 rhizobium s
15	43	51.2	406	10 Q94457	Q94457 arabidopsis
16	43	51.2	687	10 Q9LM78	Q9lm78 arabidopsis

RESULT 2
Q9VOP3 PRELIMINARY; PRT; 729 AA.
ID Q9VOP3;
AC Q9VOP3;
DT 01-MAY-2000 (TREMBLref. 13, Created)
DT 01-MAY-2000 (TREMBL. 13, Last sequence update)
DE CG3377 protein.
DE CG3377 protein.
GN E23 OR CG3327.

DEF	putative permease ABC transporter protein.
GN	R00154 OR SM02830.
OS	Rhizobium meliloti (<i>Sinorhizobium meliloti</i>); Rhizobacteria; alpha subdivision; Rhizobiaceae; <i>Sinorhizobium</i> .
OC	Bacterium; Bovinae; Bos.
NCBI_TaxID	9913;
[1]	SEQUENCE FROM N.A.
RP	MEDLINE-10219146; PubMed-10753906;
RA	Ratner A., Smallwood P.M., Nathans J.;
RT	"Identification and characterization of all-trans-retinol dehydrogenase from photoreceptor outer segments, the visual cycle enzyme that reduces all-trans-retinal to all-trans-retinol.";
J	J. Biol. Chem. 275:11034-11043 (2000).
-i	SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES (SDR) FAMILY.
CC	(EMBL: AF229846; AAF63161.1; -.
CC	HSSP: P14061; IEDBS;
DR	InterPro: IPR002198; ADH_short.
DR	Pfam: PF00106; adh_short; 1.
DR	PRINTS: PR00080; SDRFAMILY.
DR	PROSITE: PS00061; ADH_SHORT; UNKNOWN_1.
KW	Oxidoreductase; Receptor.
SEQUENCE	33936 MW; 36481039FF71874D CRC64;
Qy	53.6%; Score 45; DB 6; Length 312;
Db	Best Local Similarity 57.1%; Pred. No. 24; Mismatches 4; Indels 0; Gaps 0;
Qy	1 LKAMDPTPPLWIKT 14
Db	: :: : 268 LKAMDPTSGSLVVRT 281
RESULT 9	Q9NY761 PRELIMINARY; PRT; 125 AA.
RP	SEQUENCE FROM N.A.
ID	Q9NY761
AC	Q9NY761;
DT	01-OCT-2000 (TREMBLrel. 15, Created)
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	OVARC1000060 protein.
OS	Homo sapiens (Human).
EC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID	9606;
[1]	SEQUENCE FROM N.A.
RC	TISSUE=OVARIAN CARCINOMA;
RA	Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Ishibashi T., Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Kanehori K.,
RA	"NEO human cDNA sequencing project."
RA	Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL: AK001765; BAR91896.1; -.
SEQUENCE	125 AA; 13504 MW; F2D324918E3a70B1 CRC64;
Qy	52.4%; Score 44; DB 4; Length 125;
Db	Best Local Similarity 46.2%; Pred. No. 13; Mismatches 3; Indels 0; Gaps 0;
Qy	2 KAMDPPTPLWIKT 14
Db	: :: : 4 KSMGPPAPRMR 16
RESULT 10	Q92P32 PRELIMINARY; PRT; 377 AA.
RP	SEQUENCE FROM N.A.
ID	Q92P32
AC	Q92P32;
DT	01-DEC-2001 (TREMBLrel. 19, Created)
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE	Analysis of the chromosome sequence of the legume symbiont <i>Sinorhizobium meliloti</i> strain 1011.
DR	Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
DR	EMBL: AL591702; CAC41541.1; -.
DR	InterPro: IPR00515; BPD_transp.
DR	Pfam: PF00528; BPD_transp; 1.
KW	Complete proteome.
SEQUENCE	377 AA; 41867 MW; D8E34131C7E14415 CRC64;
Qy	6 PTPLWIKIE 15
Db	: : : 125 PTPPFWLMSE 134
RESULT 11	Q9UDG1 PRELIMINARY; PRT; 695 AA.
RP	SEQUENCE FROM N.A.
ID	Q9UDG1
AC	Q9UDG1;
DT	01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE	Submitted (MAR-2002) (TREMBLrel. 20, Last annotation update)
DE	Hypothetical protein PAB1590.
GN	PAB1590.
OS	Pyrococcus abyssi.
OC	Archaea; Euryarchaeota;
OC	Thermococci; Thermococcales; Thermococcaceae;
OX	Pyrococcus.
NCBI_TaxID	292929;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=ORSAV;
RA	Heilig R.;
RT	"Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure and evolution."
RL	Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR	EMBL: AU24826; CAB5008.1; -.
KW	Hypothetical protein; Complete proteome.
SEQUENCE	695 AA; 79999 MW; 371IE042210F551 CRC64;
Qy	52.4%; Score 44; DB 17; Length 695;
Db	Best Local Similarity 54.5%; Pred. No. 78; Mismatches 3; Indels 0; Gaps 0;
Qy	3 AMDPTPPLWIK 13
Db	:: : 561 ANDPKPMWLE 571
RESULT 12	Q15070 PRELIMINARY; PRT; 1327 AA.
RP	SEQUENCE FROM N.A.
ID	Q15070
AC	Q15070;
DT	01-JAN-1998 (TREMBLrel. 05, Created)
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT	01-JAN-1998 (TREMBLrel. 05, Last annotation update)
DE	Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR	EMBL: AL24826; CAB5008.1; -.
KW	Hypothetical protein; Complete proteome.
SEQUENCE	695 AA; 79999 MW; 371IE042210F551 CRC64;

DE	KIAA0364	protein.				
GN	KIAA0364					
OS	Homo sapiens (Human)					
OC	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Eutheria; Primates; Catarrhini; Hominidae; Homo.					
NCBI_TAXID	9606;					
OX						
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=BRAIN;					
RA	Medline=97349904; PubMed=9205641;					
RA	Nagase T., Ishikawa K., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;					
RT	*Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro.";					
DN	DNA Res. 4:141-150(1997)					
RL	DR EMBL AB002362; BAA20819; 1; -.					
RA	HSSP: P43626; INR.					
RT	InterPro: IPR03598; Ig_C2.					
DR	InterPro: IPR03600; Ig_Like.					
DR	InterPro: IPR03006; Ig_NHC.					
DR	SMART: SM00408; IgC1; 1.					
DR	SMART: SM00410; Ig_Like; 7.					
KW	Immunoglobulin domain; Ig.					
SEQUENCE	1327 AA; MW: 736C689FEC94D2E1 CRC64;					
Query Match	52.4%; Score: 44; DB 4; Length: 1327;					
Best Local Similarity	63.6%; Pred. No. 1.5e+02;					
Matches	7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;					
Qy	4 MDPTPPWIKT 14					
Db	: 25 MDPTPPWIKS 35					
RESULT 13						
Q946HB	Q946HB	PRELIMINARY;	PRT;	278 AA.		
ID	Q946HB					
AC	Q946HB:					
DT	01-DEC-2001 ("TREMBLrel. 19, Created)					
DT	01-DEC-2001 ("TREMBLrel. 19, Last sequence update)					
DT	01-MAR-2002 ("TREMBLrel. 20, Last annotation update)					
DE	Alpha-expansin.					
GN						
OS	Oryza sativa (Rice).					
OC	Eukaryota; Viridiplantae; Streptophytta; Embryophytta;					
OC	Spermatophytina; Magnoliophyta; Liliopsida; Poales; Poaceae;					
OC	Ehrhartoideae; Oryzeae; Oryzae.					
NCBI_TAXID	4530;					
OX						
RP	SEQUENCE FROM N.A.					
RX	Medline=21521059; PubMed=11641069;					
RA	Lee Y., Choi D., Kende H.,					
RT	*Expansins: ever-expanding numbers and functions. *					
RL	Curr. Opin. Plant Biol. 4:527-532(2001).					
DR	EMBL: AF34559; AAL24495; 1; -.					
DR	InterPro: IPR00882; Pollen_allergen.					
DR	Pfam: PF01357; Pollen_allergen; 1.					
DR	ProDom: PDO0219; Pollen_allergen; 1.					
SO	SEQUENCE 278 AA; 30046 MW; D70B729F091766FO CRC64;					
Query Match	51.2%; Score: 43; DB 10; Length: 278;					
Best Local Similarity	66.7%; Pred. No. 44;					
Matches	6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;					
Qy	5 DETPPWIK 13					
Db	: : 44 DETPPWIK 52					
RESULT 14						
Q8VM74						

SQ SEQUENCE 406 AA: 45986 MW: 045B92F725BD785C CRC64;
Query Match 51.2%; Score 43; DB 10; Length 406;
Best Local Similarity 46.7%; Pred. No. 65;
Matches 7; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
Qy 1 LKAMDPPPLWIKTE 15
Db | : ; | | | | :
2225 LRLLQTNPPLWIKTD 239

Search completed: June 27, 2003, 18:02:00
Job time : 31 secs